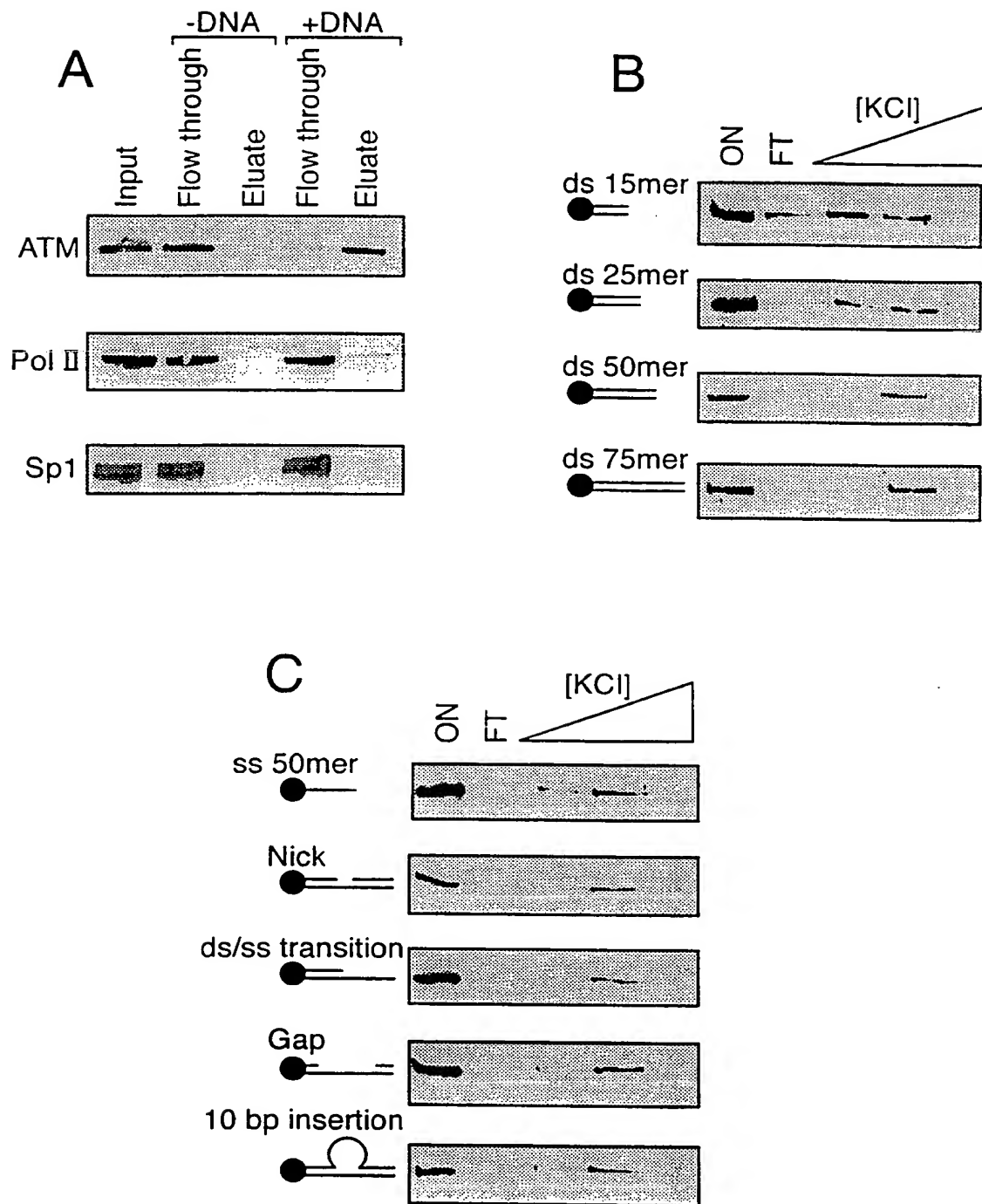


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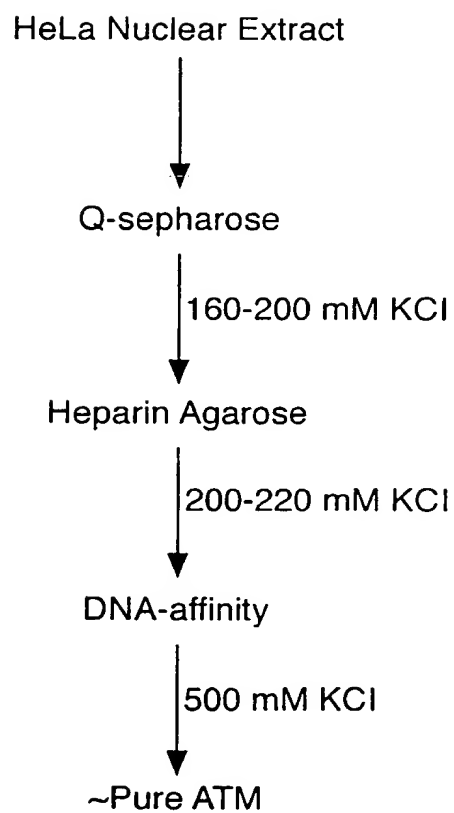
Fig.1.



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Fig.2.

A



B

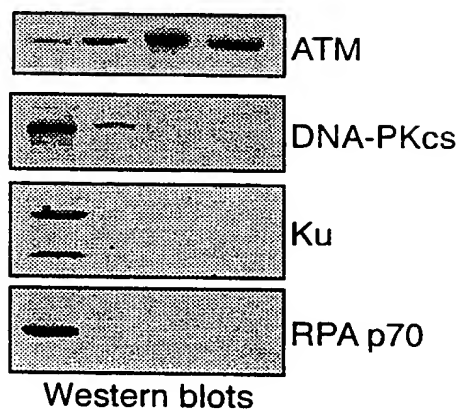
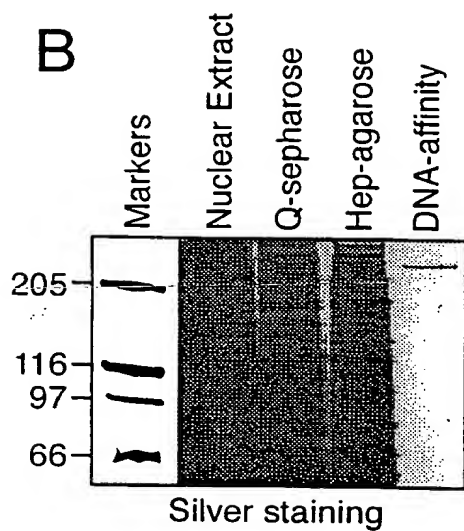
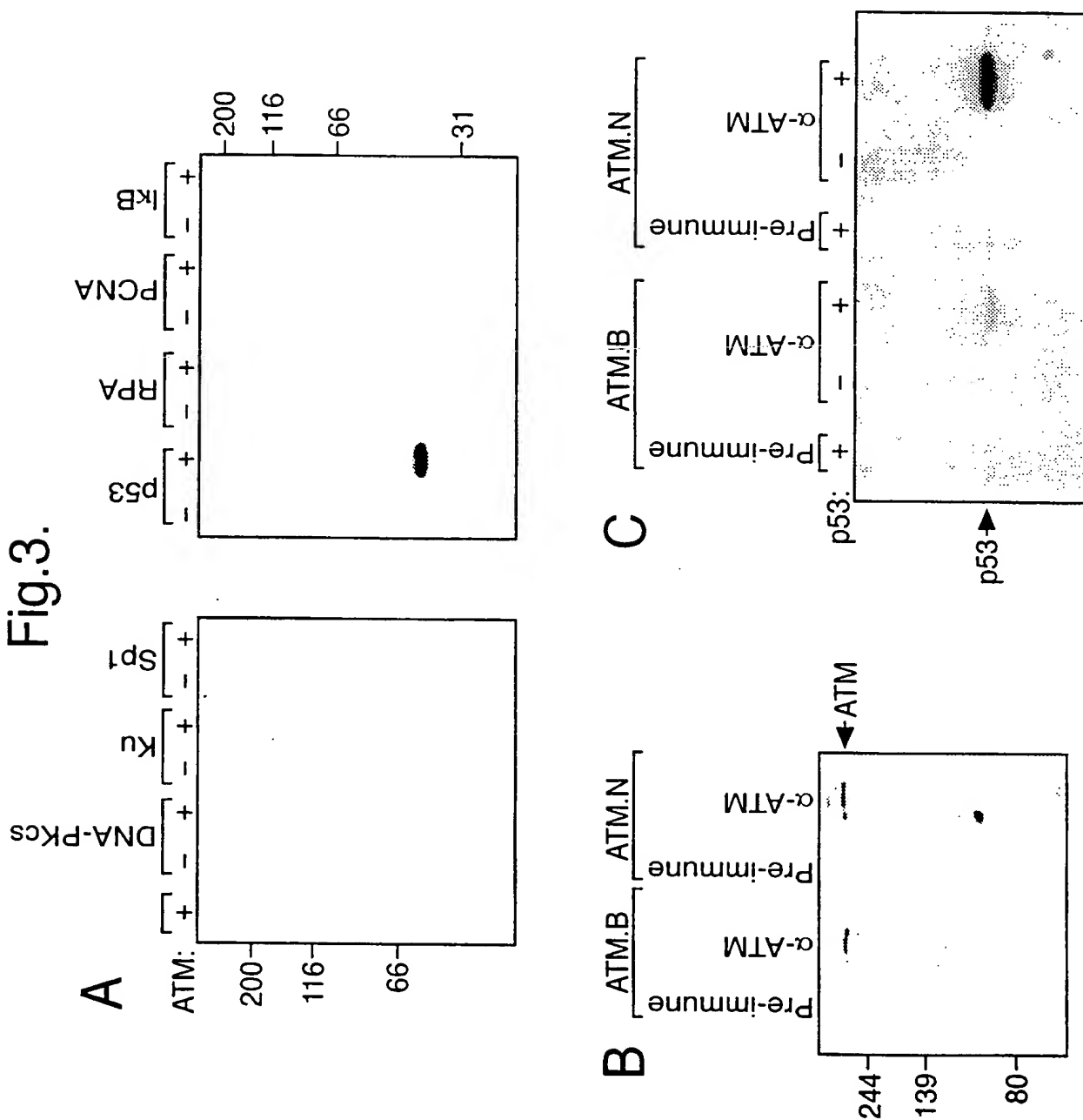
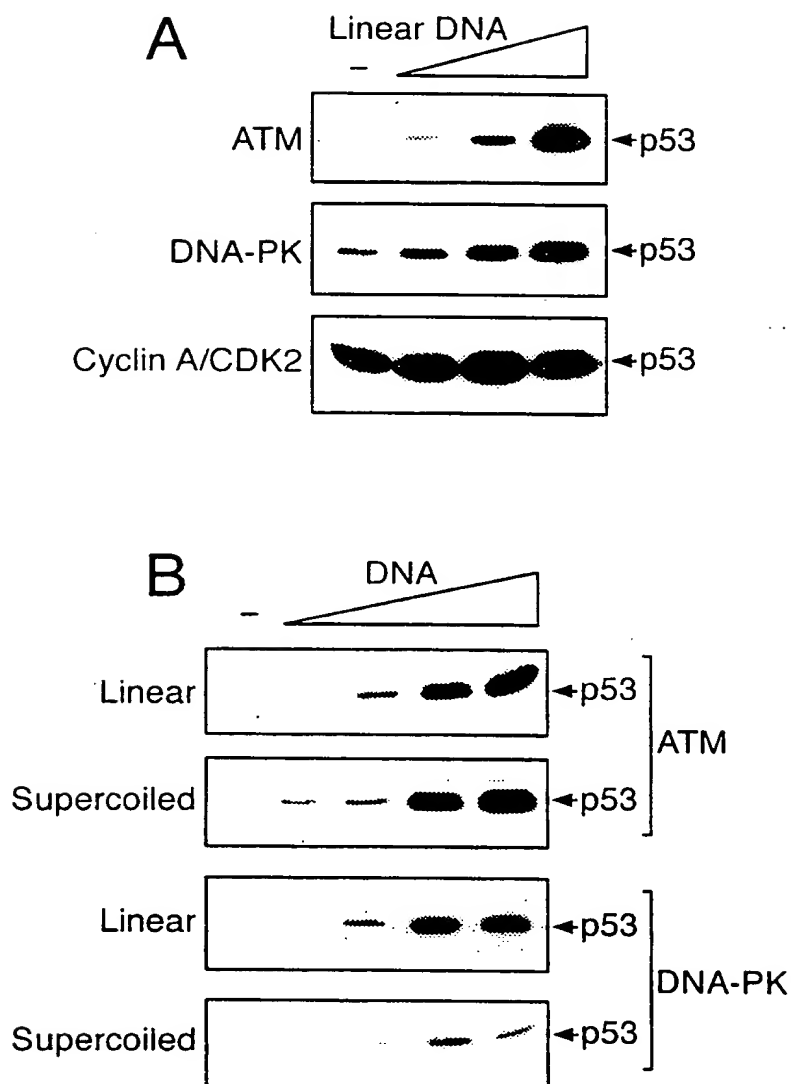


Fig.3.



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Fig.4.



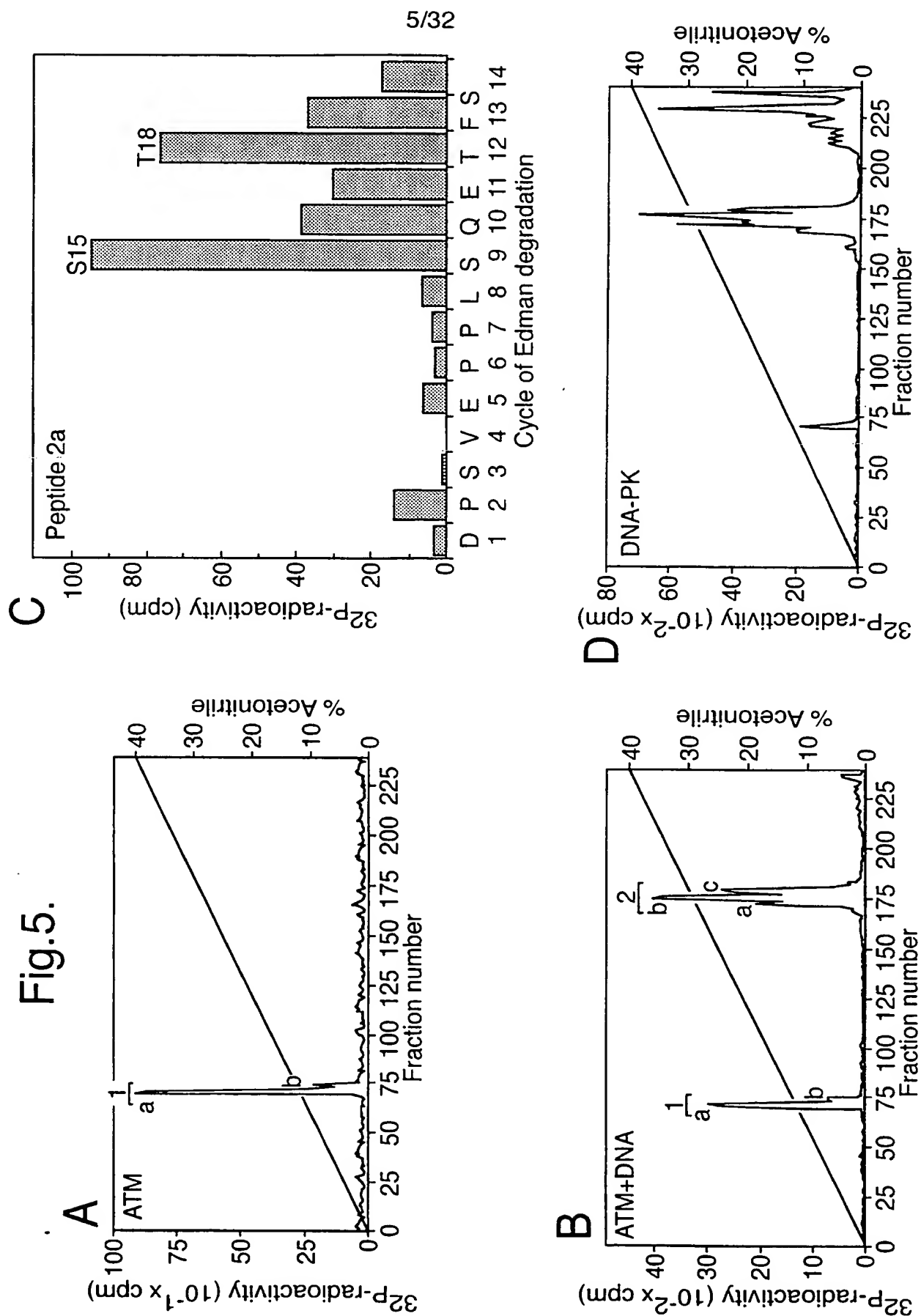


Figure 6a

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Figure 6b (1)

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Figure 6b (11)

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951 AGGAGATGAA ATTCTTCCCA CTTTGCTTTA TATTGGACT CAACATAGGC
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Figure 6 b (111)

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Figure 6b (1v)

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3701 AGGCTTTGTT TGCCCTGTGT AAATCTGTGA AAGAGAATGG ATTAGAACCT
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Figure 6b (v)

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6801 GTGGCAGAAA CACTCCCAGC TTCTCAAGGA CAGTGATTTT AGTTTTCAGG
6851 AGCCTATCAT GGCTCTACGC ACAGTCATTT TGGAGATCCT GATGGAAAAG

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Figure 6b (v1)

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7751 ACCAATTGGC TGCTAGAATG GGGACCAAGA TGATGGGAGG CCTAGGATTT
7801 CATGAAGTCC TCAATAATCT AATCTCTAGA ATTTCAATGG ATCACCCCCA
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Figure 6b (vii)

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8751  CAGTGTAGCT ACTTCTTCTA TTGTTGGTTA CATACTTGGG CTTGGTGATA
8801  GACATGTACA GAATATCTTG ATAAATGAGC AGTCAGCAGA ACTTGTACAT
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8901  GACAGTTCTT TTTAGACTCA CCAGAGATAT TGTGGATGGC ATGGGCATTA
8951  CGGGTGTGTA AGGTGTCTTC AGAAGATGCT GTGAGAAAAC CATGGAAGTG
9001  ATGAGAAACT CTCAGGAAAC TCTGTTAACC ATTGTAGAGG TCCTTCTATA
9051  TGATCCACTC TTTGACTGGA CCATGAATCC TTTGAAAGCT TTGTATTTAC
9101  AGCAGAGGCC GGAAGATGAA ACTGAGCTTC ACCCTACTCT GAATGCAGAT
9151  GACCAAGAAT GCAAACGAAA TCTCAGTGAT ATTGACCAGA GTTTCGACAA
9201  AGTAGCTGAA CGTGTCTTAA TGAGACTACA AGAGAACTG AAAGGAGTGG
9251  AAGAAGGCAC TGTGCTCAGT GTTGGTGGAC AGGTGAATTT GCTCATACAG
9301  CAGGCCATAG ACCCAAAAAA TCTCAGCCGA CTTTTCCTCAG GATGGAAAGC
9351  TTGGGTGTGA TCTTCAGTAT ATGAATTACC CTTTC
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Figure 7a

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FT                          KQSQHMTEVVRRCPHHERCSDSDGLAPPQHLIRVEGNLRVEYLDDRNTFRHSVVVPYEP
FT                          PEVGSDCTTIHYNMCMSSCMGGMNRRPILTIITLEDSSGNLLGRNSFEVVRVCACPGRD
FT                          RRTEENLRKKGEPHHELPPGSTKRALPNNTSSSPQPKKKPLDGEYFTLQIRGRERFEM
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SQ   Sequence 1303 BP; 292 A; 403 C; 348 G; 260 T; 0 other;

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M14695 Length: 1303 July 10, 1998 12:29 Type: N Check: 4902 ..

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151 CGAGCCCCCT CTGAGTCAGG AAACATTTTC AGACCTATGG AAATACTTTC
201 CTGAAAACAA CGTTCTGTCC CCCTTGCCGT CCCAAGCAAT GGATGATTTG
251 ATGCTGTCCC CGGACGATAT TGAACAATGG TTCACTGAAG ACCCAGGTCC

```

Figure 7b (1)

Figure 7b (11)

301 AGATGAAGCT CCCAGAATGC CAGAGGCTGC TCCCCCGTG GCCCCTGCAC
351 CAGCGACTCC TACACCGGCG GCCCCTGCAC CAGCCCCCTC CTGGCCCCCTG
401 TCATCTTCTG TCCCTTCCCA GAAAACCTAC CAGGGCAGCT ACGGTTTCCG
451 TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT
501 CCCCTGCCCT CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG
551 CAGCTGTGGG TTGATTCCAC ACCCCCGCCC GGCACCCGCG TCCGCGCCAT
601 GGCCATCTAC AAGCAGTCAC AGCACATGAC GGAGGTTGTG AGGCGCTGCC
651 CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC TCCTCAGCAT
701 CTTATCCGAG TGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA
751 CACTTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT
801 CTGACTGTAC CACCATCCAC TACAACCTACA TGTGTAACAG TTCTGTCATG
851 GGCGGCATGA ACCGGAGGCC CATCCTCACC ATCATCACAC TGAAGACTC
901 CAGTGTAAT CTACTGGGAC GGAACAGCTT TGAGGTGCGT GTTTGTGCCT
951 GTCTGGGAG AGACCGGCGC ACAGAGGAAG AGAATCTCCG CAAGAAAGGG
1001 GAGCCTCACC ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCCAA
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1151 CTGAATGAGG CCTTGGAACCT CAAGGATGCC CAGGCTGGGA AGGAGCCAGG
1201 GGGGAGCAGG GCTCACTCCA GCCACCTGAA GTCCAAAAAG GGTCAGTCTA
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1301 TGA

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Figure 8a (i)

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!!NA_SEQUENCE 1.0
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DT   20-MAY-1996 (Rel. 47, Last updated, Version 1)
XX
-> DE   Human FRAP-related protein (FRP1) mRNA, complete cds.
XX
KW
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates;
OC   Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-8210
RA   Cimprich K.A., Shin T.B., Keith C.T., Schreiber S.L.;
RT   "cDNA cloning and gene mapping of a candidate human cell cycle
RT   checkpoint protein";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:2850-2855(1996).
XX
RN   [2]
RP   1-8210
RA   Cimprich K.A., Shin T.B., Keith C.T., Schreiber S.L.;
RT   ;
RL   Submitted (22-FEB-1996) to the EMBL/GenBank/DDBJ databases.
RL   Karlene A. Cimprich, Chemistry, Harvard University, 12 Oxford Street,
RL   Cambridge, MA 02138, USA
XX
DR   SPTREMBL; Q13535; Q13535.
XX
FH   Key          Location/Qualifiers
FH
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FT                   /chromosome="3"
FT                   /cell_type="Jurkat T-cell"
FT                   /map="3q22-q24"
FT   CDS             106. .8040
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FT                   /db_xref="SPTREMBL:Q13535"
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FT                   /product="FRAP-related protein"
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FT                   TRLLRIAATPSCHLLHKKICEVICSLFLFKSKSPAIFGVLTKEQLQLFEDLVYLHRRN
FT                   VMGHAVEVPVMSRFLSQLDEHMGYLOSAPIQLMSQNLFEIVTLIMVLTRI IATVFF
FT                   RRQELLLWQIGCVLLEYGSPKIKSLAISFLTQLGGLPAQPASTFFSFLLELLKHLV
FT                   EMDTDQLKLYEPEPLSKLIKTLFPFEAEAYRNIEPVYLANMLEKLCVMFEDGVLMRLKSD
FT                   LLKAALCHLLQYFLKFVPAGYESALQVRKVYVRNICKALLDVLGIEVDAEYLLGPLYAA
FT                   LKMESEMEIEEIQCQTQENLSSNSDGISPKRRRLSSSLNPSKRAPKQTEELKHVDMNQ
FT                   KSILWSALKQKAESLQISLEYSGLKNPVIEMLEGIADVVLQLTALCTVHCSHQNMNCRTF
FT                   KDCQHKSKKKPSVVTWMSLDFYTKVLKSCRSLLSVQKLDLEATIDKVVKIYDALIYM
FT                   QVNSSFEDHILEDLCGMLSPLWTYSHSDDGCLKLTTFANLLTLSCRISDSYSPOAQR
FT                   CVFLLTLFPFRIIFLEWRTAVYNWALQSSHEVIRASCVSQGFILLQQQNSCNRVVKILID
FT                   KVKDDSDIVKKEFASILGQVLCTLHGMFYLTSSLTEPFSEGHVDFLCRNKATSQHEC
FT                   SSSQLKASVCKPFLFLLKKKIPSPVKLAFIDNLHHLCKHLDFREDETQVAVLGTLLNL
FT                   MEDPDKDVRVAFSGNIKHILESLSDEDFIKELFVLRMKEAYTHAQISRNNELKDTLLIL
FT                   TTGDIGRAAKGDLVPFALLHLHCLLSKKSASVSGAAYTEIRALVAKSVKIQSFFSQYK
FT                   KPICQFLVESLHSSQMTALPNTPCQNAQVVRKQDVAHQREMAIINTLSEIANVDFDPDLNR
FT                   FLTRTLQVLLPDLAASKASPAASALIRTLGKQLNVNRREILINNFKYIFSHLVCSCSKDE

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Figure 8a (11)

FT LERALHYLKNETEIELGSLLRQDFQGLHNEILLRIGEHYQOVFNGLSILASFASSDDPY
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 FT VSSVRVKMMTTTLRTGLRFKDDFPELCCRAWDCFVRCLDHACLSLLSHVIVALLPLIHI
 FT QPKETAAIFHYLIENRDAVQDFLHEIYFLPDHPELKKIKAVLQYRKETSESTDLQTT
 FT LQLSMKAIQHENVVRIHALTSLKETLYKNQEKLIKYATDSETVEPIISQLVTVLLKGC
 FT QDANSQARLLCGECLGELGAIDPGRLDFTTETQGKDFTFVTGVEDSSFAYGLLMELTR
 FT AYLAYADNSRAQDSAAAYAIQELLSIYDCREMETNGPGHQLWRRFPHEVREILEPHLNTR
 FT YKSSQKSTDSGKVKPIYLSKLGSNFAEWSASWAGYLITKVRHDLASKIFTCCSIMMKH
 FT DFKVTIYLLPHILVYVLLGCGNQEDQOEYAEIMAVLKHDDQHTINTQDIASDLQQLSTQ
 FT TVFSMLDHLTQWARHKFQALKAKECPHKSNNRNVKDSMVSTVDYEDYQSVTRFLDLIPQ
 FT TFLAVASFRSKAYTRAVMHFESFITEKKQNIQEHLGFLQKLYAAMHEPDGVAGVSAIRK
 FT AEPSLKEQILEHESLGLLRDATAICYDRAIQLEPDQIIHYHGVVKSMLGLGQLSTVITQV
 FT NGVHANRSEWTDELNTYRVEAAWKLQWDLVENYLAADGKSTTWSVRLGQLLLSAAKRD
 FT ITAFYDSLKLVRAEQIVPLSAASFERSYQRYEYIVRLHMLCEHSIKPLFQHSPGD
 FT SSQEDSLNWWARLEMTQNSYRAKEPILALRRALLSLNKRDPDYNEMVGECLWQSARVARK
 FT AGHHQTAYNALLNAGESRLAELYVERAKWLWSKGDVHQAIVLQKVELCFPENETPPE
 FT GKNNMLIHGRAMLLVGRFMEETANFESNAIMKKYKDVTAACLPWEDEGHFYLAQYDKLMP
 FT MVTDNKMEKQGDILIRYIVLHFGSRSLQYGNQFIYQSMRMLTLWLVDYGTAYEWKAGRS
 FT DRVQMRNDLGKINKYVTEHTNYLAPYQFLTAQSILSRICHSHDEVFVLMELIAKVF
 FT AYPQQAMMMMTAVSKSSYPMRVNRCKEILNKAHMKKSLEKFGDATRLTDKLELGNK
 FT PVDGSSSTLSMSTHFKMLKLVVEEATFSEILIPQSVMIPTLPSILGTHANHASHEPFP
 FT GHWAYIAGFDDMVEILASLQKPKKISLKGSDGKFYIMMCKPKDDLKDCRLMEFNSLIN
 FT KCLRKDAESRRRELHIRTAVIPLNDECGIIEWVNNTAGLRPILTKLYKEGVYMTGKE
 FT LRQCMPLPKSAALSEKLVFRELLPRHPPIFHEWFLRTFPDPTSWYSSRSAYCRSTAVM
 FT SMVGYILGLGDRHGENILFDSLGTGECVHVDNCLFNKGETFEVPEIVPFRLLTHNMVNGM
 FT GPMGTGELFRACEVTMLMRDQREPLMSVLKTFHLDPLVEWSKPVKGHSKAPLNETGE
 FT VVNEKAKTHVLDIEQRLQGVIKTRNRVTGLPLSIEGHVHYLIEATDENLLCQMYLGWT
 FT PYM*
 XX
 SQ Sequence 8210 BP; 2511 A; 1555 C; 1738 G; 2406 T; 0 other;

U49844 Length: 8210 July 10, 1998 12:08 Type: N Check: 4511 ..

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 51 TGGAGACGCC GGAACCCGC GTTGGCGTGG TTGACTAGTG CCTCGCAGCC
 101 TCAGCATGGG GGAACATGGC CTGGAGCTGG CTTCCATGAT CCCC GCCCTG
 151 CGGGAGCTGG GCAGTGCCAC ACCAGAGGAA TATAATACAG TTGTACAGAA
 201 GCCAAGACAA ATTCTGTGTC AATTCATIGA CCGGATACTT ACAGATGTAA
 251 ATGTTGTTGC TGTAGAACTT GTAAAGAAAA CTGACTCTCA GCCAACCTCC
 301 GTGATGTTGC TTGATTTTCAT CCAGCATATC ATGAAATCCT CCCC ACTTAT
 351 GTTTGTAAAT GTGAGTGGAA GCCATGAGGC CAAAGGCAGT TGTATTGAAT
 401 TCAGTAATTG GATCATAACG AGACTTCTGC GGATTGCAGC AACTCCCTCC
 451 TGTCAATTTGT TACACAAGAA AATCTGTGAA GTCATCTGTT CATTATTATT
 501 TCTTTTTTAAA AGCAAGAGTC CTGCTATTTT TGGGGTACTC ACAAAGAAT
 551 TATTACAAC TTTTGAAGAC TTGGTTTACC TCCATAGAAG AAATGTGATG
 601 GGTGATGCTG TGGAAATGGC AGTGGTCATG AGCCGATTTT TAAGTCAATT
 651 AGATGAACAC ATGGGATATT TACAATCAGC TCCTTTGCAG TTGATGAGTA
 701 TGCAAAATTT AGAATTTATT GAAGTCACTT TATTAATGGT TCTTACTOGT
 751 ATTATTGCAA TTGTGTTTTT TAGAAGGCAA GAACTCTTAC TTTGGCAGAT
 801 AGGTTGTGTT CTGCTAGAGT ATGGTAGTCC AAAAAATTAAA TCCCTAGCAA

Figure 8b(1)

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Figure 8b (ii)

851 TTAGCTTTTT AACAGAACTT TTTCAGCTTG GAGGACTACC AGCACAACCA
901 GCTAGCACTT TTTTCAGCTC ATTTTGGAA TTATTAAAAC ACCTTGTTAGA
951 AATGGATACT GACCAATTGA AACTCTATGA AGAGCCATTA TCAAAGCTGA
1001 TAAAGACACT ATTTCCCTTT GAAGCAGAAG CTTATAGAAA TATTGAACCT
1051 GTCTATTTAA ATATGCTGCT GGAAAACTC TGTGTCATGT TTGAAGACGG
1101 TGTGCTCATG CGGCTTAAGT CTGATTTGCT AAAAGCAGCT TTGTGCCATT
1151 TACTGCAGTA TTTCCCTTAA TTTGTGCCAG CTGGGTATGA ATCTGCTTTA
1201 CAAGTCAGGA AGGTCTATGT GAGAAATATT TGTAAGCTC TTTTGGATGT
1251 GCTTGGAAAT GAGGTAGATG CAGAGTACTT GTTGGGCCCA CTTTATGCAG
1301 CTTTGAAAAT GGAAAGTATG GAAATCATTG AGGAGATTCA ATGCCAACT
1351 CAACAGGAAA ACCTCAGCAG TAATAGTGAT GGAATATCAC CCAAAGGCG
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1451 AGGAAATTAA ACATGTGGAC ATGAACCAA AGAGCATATT ATGGAGTGCA
1501 CTGAAACAGA AAGCTGAATC CCTTCAGATT TCCCTTGAAT ACAGTGGCCT
1551 AAAGAATCCT GTTATTGAGA TGTTAGAAGG AATTGCTGTT GTCTTACAAC
1601 TGA CTGCTCT GTGTACTGTT CATTTGTTCTC ATCAAAACAT GAACTGCCGT
1651 ACTTTCAAGG ACTGTCAACA TAAATCCAAG AAGAAACCTT CTGTAGTGAT
1701 AACTTGGATG TCATTGGATT TTTACACAAA AGTGCTTAAG AGCTGTAGAA
1751 GTTTGTTAGA ATCTGTTTCA AACTGGACC TGGAGGCAAC CATTGATAAG
1801 GTGGTGAAAA TTTATGATGC TTTGATTTAT ATGCAAGTAA ACAGTTTATT
1851 TGAAGATCAT ATCCTGGAAG ATTTATGTGG TATGCTCTCA CTTCCATGGA
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2251 TGTACTCTTC ACGGCATGTT TTATCTGACA AGTTCTTTAA CAGAACCTTT
2301 CTCTGAACAC GGACATGTGG ACCTCTTCTG TAGGAACCTG AAAGCCACTT
2351 CTCAACATGA ATGTTTATCT TCTCAACTAA AAGCTTCTGT CTGCAAGCCA
2401 TTCTTTTCC TACTGAAAAA AAAATACCT AGTCCAGTAA AACTTGCTTT
2451 CATAGATAAT CTACATCATC TTTGTAAGCA TCTTGATTTT AGAGAAGATG
2501 AAACAGATGT AAAAGCAGTT CTTGGAACCT TATTAAATTT AATGGAAGAT

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Figure 8b (111)

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2651 GAATGAAGGA AGCATATACA CATGCCCAA TATCAAGAAA TAATGAGCTG
2701 AAGGATACCT TGATTCCTAC AACAGGGGAT ATTGGAAGGG CCGCAAAAGG
2751 AGATTTGGTA CCATTTGCAC TCTTACACTT ATTGCATTGT TTGTTATCCA
2801 AGTCAGCATC TGTCTCTGGA GCAGCATACA CAGAAATTAG AGCTCTGGTT
2851 GCAGCTAAAA GTGTTAAACT GCAAAGTTTT TTCAGCCAGT ATAAGAAACC
2901 CATCTGTCAG TTTTTGGTAG AATCCCTTCA CTCTAGTCAG ATGACAGCAC
2951 TTCCGAATAC TCCATGCCAG AATGCTGACG TCGGAAAACA AGATGTGGCT
3001 CACCAGAGAG AAATGGCTTT AAATACGTTG TCTGAAATTG CCAACGTTTT
3051 CGACTTTCCT GATCTTAATC GTTTCTTAC TAGGACATTA CAAGTTCTAC
3101 TACCTGATCT TGCTGCCAAA GCAAGCCCTG CAGCTTCTGC TCTCATTCGA
3151 ACTTTAGGAA AACAATTAAA TGTCAATCGT AGAGAGATTT TAATAAACAA
3201 CTTCAAATAT ATTTTTTCTC ATTTGGTCTG TTCTTGTTCC AAAGATGAAT
3251 TAGAACGTGC CCTTCATTAT CTGAAGAATG AAACAGAAAT TGAAGTGGGG
3301 AGCCTGTTGA GACAAGATTT CCAAGGATTG CATAATGAAT TATTGCTGCG
3351 TATTGGAGAA CACTATCAAC AGGTTTTTAA TGGTTTGTC AACTTTGCCT
3401 CATTTGCATC CAGTGATGAT CCATATCAGG GCCCAGAGA TATCATATCA
3451 CCTGAACTGA TGGCTGATTA TTTACAACCC AAATTGTTGG GCATTTTGGC
3501 TTTTTTTAAC ATGCAGTTAC TGAGCTCTAG TGTGGCATT GAAGATAAGA
3551 AAATGGCCTT GAACAGTTTG ATGTCCTTGA TGAAGTTAAT GGGACCCAAA
3601 CATGTCAGTT CTGTGAGGGT GAAGATGATG ACCACACTGA GAACTGGCCT
3651 TCGATTCAAG GATGATTTTC CTGAATTGTG TTGCAGAGCT TGGGACTGCT
3701 TTGTTGCTG CCTGGATCAT GCTTGTCTGG GCTCCCTTCT CAGTCATGTA
3751 ATAGTAGCTT TGTTACCTCT TATACACATC CAGCCTAAAG AAAGTGCAGC
3801 TATCTTCCAC TACCTCATAA TTGAAAACAG GGATGCTGTG CAAGATTTTC
3851 TTCATGAAAT ATATTTTTTA CCTGATCATC CAGAATTAAA AAAGATAAAA
3901 GCGTTTCTCC AGGAATACAG AAAGGAGACC TCTGAGAGCA CTGATCTTCA
3951 GACAACTCTT CAGCTCTCTA TGAAGGCCAT TCAACATGAA AATGTGATG
4001 TTGCTATTCA TGCTCTTACA AGCTTGAAGG AAACCTTGTA TAAAAATCAG
4051 GAAAACTGA TAAAGTATGC AACAGACAGT GAAACAGTAG AACCTATTAT
4101 CTCACAGTTG GTGACAGTGC TTTTGAAAGG TTGCCAAGAT GCAAACTCTC
4151 AAGCTGGTT GCTCTGTGGG GAATGTTTAG GGAATTGGG GCGATAGAT

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Figure 8b (iv)

4201 CCAGGTCGAT TAGATTTCTC AACAACTGAA ACTCAAGGAA AAGATTTTAC
4251 ATTTGTGACT GGAGTAGAAG ATTCAAGCTT TGCCTATGGA TTATTGATGG
4301 AGCTAACAAAG AGCTTACCTT GCGTACGCTG ATAATAGCCG AGCTCAAGAT
4351 TCAGCTGCCT ATGCCATTCA GGAGTTGCTT TCTATTTATG ACTGTAGAGA
4401 GATGGAGACC AACGGCCCAG GTCACCAATT GTGGAGGAGA TTTCCTGAGC
4451 ATGTTGGGA AATACTAGAA CCTCATCTAA ATACCAGATA CAAGAGTTCT
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4751 ATGCAGAAAT TATGGCAGTT CTAAAGCATG ACGATCAGCA TACCATAAAT
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4851 CTCCATGCTT GACCATCTCA CACAGTGGGC AAGGCACAAA TTTCAGGCAC
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4951 TCAATGGTAT CTA CTGTGGA TTATGAAGAC TATCAGAGTG TAACCCGTTT
5001 TCTAGACCTC ATACCCCAGG ATACTCTGGC AGTAGCTTCC TTTCGCTCCA
5051 AAGCATACAC ACGAGCTGTA ATGCACTTTG AATCATTTAT TACAGAAAAG
5101 AAGCAAAATA TTCAGGAACA TCTTGGATTT TTACAGAAAT TGTATGCTGC
5151 TATGCATGAA CCTGATGGAG TGGCCGGAGT CAGTGCAATT AGAAAGGCAG
5201 AACCATCTCT AAAAGAACAG ATCCTTGAAC ATGAAAGCCT TGGCTTGCTG
5251 AGGGATGOCA CTGCTTGTTA TGACAGGGCT ATTCTAGCTAG AACCAGACCA
5301 GATCATTCAT TATCATGGTG TAGTAAAGTC CATGTTAGGT CTGGTCAGC
5351 TGTCTACTGT TATCACTCAG GTGAATGGAG TGCATGCTAA CAGGTCCGAG
5401 TGGACAGATG AATTAAACAC GTACAGAGTG GAAGCAGCTT GGAAATTGTC
5451 ACAGTGGGAT TTGGTGGAAA ACTATTTGGC AGCAGATGGA AAATCTACAA
5501 CATGGAGTGT CAGACTGGGA CAGCTATTAT TATCAGCCAA AAAAAGAGAT
5551 ATCAGAGCTT TTTATGACTC ACTGAAACTA GTGAGAGCAG AACAAATTGT
5601 ACCTCTTTCA GCTGCAAGCT TTGAAAGAGG CTCTACCAA CGAGGATATG
5651 AATATATTGT GAGATTGCAC ATGTTATGTG AGTTGGAGCA TAGCATCAAA
5701 CCACCTTTC AGCATCTCC AGGTGACAGT TCTCAAGAAG ATTCTCTAAA
5751 CTGGGTAGCT CGACTAGAAA TGACCCAGAA TTCTACAGA GCCAAGGAGC
5801 CTATCTGGC TCTCCGGAGG GCTTTACTAA GCTCAACAA AAGACCAGAT
5851 TACAATGAAA TGGTTGGAGA ATGCTGGCTG CAGAGTGOCA GGGTAGCTAG

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Figure 8b (v)

5901 AAAGGCTGGT CACCACCAGA CAGCCTACAA TGCTCTCCTT AATGCAGGGG
5951 AATCACGACT CGCTGAACTG TACGTGGAAA GGGCAAAGTG GCTCTGGTCC
6001 AAGGGTGTATG TTCACCAGGC ACTAATTGTT CTTCAAAAAG GTGTTGAATT
6051 ATGTTTTCCT GAAAATGAAA CCCACCTGA GGGTAAGAAC ATGTTAATCC
6101 ATGGTCGAGC TATGCTACTA GTGGGCCGAT TTATGGAAGA AACAGCTAAC
6151 TTTGAAAGCA ATGCAATTAT GAAAAATAT AAGGATGTGA CCGCGTGCCT
6201 GCCAGAATGG GAGGATGGGC ATTTTACCT TGCCAAGTAC TATGACAAAT
6251 TGATGCCCCAT GGTACAGAC AACAAAATGG AAAAGCAAGG TGATCTCATC
6301 CGGTATATAG TTCTTCATTT TGGCAGATCT CTACAATATG GAAATCAGTT
6351 CATATATCAG TCAATGCCAC GAATGTTAAC TCTATGGCTT GATTATGGTA
6401 CAAAGGCATA TGAATGGGAA AAAGCIGGCC GCTCCGATCG TGTACAAATG
6451 AGGAATGATT TGGGTAAAAT AAACAAGGTT ATCACAGAGC ATACAAACTA
6501 TTTAGCTCCA TATCAATTTT TGA CTGCTTTT TTCACAATTG ATCTCTCGAA
6551 TTTGTCAATC TCACGATGAA GTTTTGTGTG TCTTGATGGA AATAATAGCC
6601 AAAGTATTTT TAGCCTATCC TCAACAAGCA ATGTGGATGA TGACAGCTGT
6651 GTCAAAGTCA TCTTATCCCA TGCGTGTGAA CAGATGCAAG GAAATCCTCA
6701 ATAAAGCTAT TCATATGAAA AAATCCTTAG AGAAGTTTGT TGGAGATGCA
6751 ACTCGCCTAA CAGATAAGCT TCTAGAATTG TGCAATAAAC CGGTTGATGG
6801 AAGTAGTTCC ACATTAAGCA TGAGCACTCA TTTTAAAATG CTTAAAAAGC
6851 TGGTAGAAGA AGCAACATTT AGTGAAATCC TCATTCTCTT ACAATCAGTC
6901 ATGATACCTA CACTTCCATC AATTCTGGGT ACCCATGCTA ACCATGCTAG
6951 CCATGAACCA TTCTCTGGAC ATTGGGCCTA TATTGCAGGG TTTGATGATA
7001 TGGTGGAAAT TCTTGCTTCT CTTCAGAAAC CAAAGAAGAT TTCTTTAAAA
7051 GGCTCAGATG GAAAGTTCTA CATCATGATG TGTAAGCCAA AAGATGACCT
7101 GAGAAAGGAT TGTAGACTAA TGGAATTCAA TTCCTTGATT AATAAGTGCT
7151 TAAGAAAAGA TGCAGAGTCT CGTAGAAGAG AACTTCATAT TCGAACATAT
7201 GCAGTTATTC CACTAAATGA TGAATGTGGG ATTATTGAAT GGGTGAACAA
7251 CACTGCTGGT TTGAGACCTA TTCTGACCAA ACTATATAAA GAAAAGGGAG
7301 TGTATATGAC AGGAAAAGAA CTTGCGCAGT GTATGCTACC AAAGTCAGCA
7351 GCTTTATCTG AAAAATCAA AGTATTCCGA GAATTTCTCC TGCCAGGCA
7401 TCCTCTATT TTTCAATGAGT GGTTCCTGAG AACATTCCCT GATCCTACAT
7451 CATGGTACAG TAGTAGATCA GCTTACTGCC GTTCCACTGC AGTAATGTCA
7501 ATGGTTGGTT ATATTCTGGG GCTTGGAGAC CGTCATGGTG AAAATATTCT

Figure 8b (v1)

7551 CTTTGATTCT TTGACTGGTG AATGCGTACA TGTAGATTTC AATTGTCTTT
7601 TCAATAAGGG AGAAACCTTT GAAGTTCCAG AAATTGTGCC ATTTCCGCTG
7651 ACTCATAATA TGGTTAATGG AATGGGTCCT ATGGGAACAG AGGGTCTTTT
7701 TCGAAGAGCA TGTGAAGTTA CAATGAGGCT GATGCGTGAT CAGCGAGAGC
7751 CTTTAATGAG TGTCTTAAAG ACTTMTCTAC ATGATCCTCT TGTGGAATGG
7801 AGTAAACCAG TGAAAGGGCA TTCCAAAGCG CCACTGAATG AAAGTGGAGA
7851 AGTTGTCAAT GAAAAGGCCA AGACCCATGT TCTTGACATT GAGCAGCGAC
7901 TACAAGGTGT AATCAAGACT CGAAATAGAG TGACAGGACT GCCGTATCT
7951 ATTGAAGGAC ATGTGCATTA CCTTATACAG GAAGCTACTG ATGAAAACCT
8001 ACTATGCCAG ATGTATCTTG GTTGGACTCC ATATATGTGA AATGAAATTA
8051 TGTAAGAGAA TATGTTAATA ATCTAAAAGT AATGCATTTG GTATGAATCT
8101 GTGGTTGTAT CTGTTCAATT CTAAAGTACA ACATAAATTT ACGTTCACAG
8151 CAACTGTTAT TTCTCTCTGA TCATTAATTA TATGTAAAAT AATATACATT
8201 CACTCGTGCC

Figure 9a (1)

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!!NA_SEQUENCE 1.0
ID   HS349941   standard; RNA; HUM; 12780 BP.
XX
AC   U34994;
XX
NI   g995940
XX
DT   26-SEP-1995 (Rel. 45, Created)
DT   22-FEB-1997 (Rel. 51, Last updated, Version 4)
XX
DE   Human DNA-dependent protein kinase catalytic subunit (DNA-PKcs)
DE   mRNA, complete cds.
XX
KW
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates;
OC   Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-12780
RX   MEDLINE; 95401275.
RA   Hartley K.O., Gell D., Smith G.C., Zhang H., Divecha N., Connelly M.A.,
RA   Admon A., Lees-Miller S.P., Anderson C.W., Jackson S.P.;
->RT   "DNA-dependent protein kinase catalytic subunit: a relative of
RT   phosphatidylinositol 3-kinase and the ataxia telangiectasia gene
RT   product";
RL   Cell 82:849-856(1995).
XX
RN   [2]
RP   1-12780
RA   Gell D.;
RT   ;
RL   Submitted (29-AUG-1995) to the EMBL/GenBank/DDBJ databases.
RL   Dave Gell, Zoology, Wellcome/CRC, Tennis Court Road, Cambridge CB2 1QR,
RL   UK
XX
DR   SPTREMBL; Q13327; Q13327.
XX
CC   NCBI gi: 995940
XX
FH   Key          Location/Qualifiers
FH
FT   source          1. .12780
FT                   /organism="Homo sapiens"
FT                   /chromosome="8"
FT                   /cell_type="He-La"
FT                   /map="8q11"
FT   CDS             53. .12343
FT                   /codon_start=1
FT                   /db_xref="PID:g995941"
FT                   /db_xref="SPTREMBL:Q13327"
FT                   /note="DNA-activated protein kinase catalytic subunit; PI
FT                   kinase family member; partial genomic sequence located in
FT                   GenBank Accession Number L27425; Method: conceptual
FT                   translation supplied by author. NCBI gi: 995941"
FT                   /gene="DNA-PKcs"
FT                   /product="DNA dependent protein kinase catalytic subunit"
FT                   /translation="MAGSGAGVRCSSLRLQETLSAADRCGAALAGHQLIRGLGQECVLS
FT                   SSPAVLALQTSLVFSDFGLLVVFVRKSLNSIEFRECREEILKFLCIFLEKMGQKIAPYS
FT                   VEIKNTCTSVYTKDRAAKCKIPALDLLIKLLQTFRSSRLMDEFKIGELFSKFYGELALK
FT                   KKIPDTVLEKVVYELLGGLGEVHPSEMINNAENLFRAFLGELKTQMTSAVREPKLPLVLAG
FT                   CLKGLSSLLCNFTKSMEEDPQTSREIFNFVLKAIRPQIDLKRYAVPSAGLRLFALHASQ
FT                   FSTCLLDNYVSLFEVLLKWCAGHTNVELKKAALSALESFLKQVSNMVAKNAEMHKNKLOY
FT                   FMEQFYGIIRNVDSNNKELSLAIRGYGLFAGPCKVINAKDVFMYVELIQRCCKQMFLLQ
FT                   TDTGDIRVYQMPFSLQSVASVLLYLDTVPEVYTFVLEHLVVMQIDSFQYSPKMQLVCC
FT                   RAIVKVFLAALAKGPVLRNCISTVHHQGLIRICSKPVVLPKGPESESEDHRASGEVRTG

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Figure 9 (ii)

FT KWKVPTYKDYVDLFRHLLSSDQMDSILADEAFFSVNSSSESLNHLLYDEFVKSVLKIV
 FT EKLDLTLEIQTVGEQENGDEAPGVWMIPTSDPAANLHPAKPKDFSANLVEFCREILP
 FT EKQAEFFEPWVYSFSYELILQSTRPLISGFYKLLSITVRNAKKIKYFEGVSPKSLKHS
 FT PEDPEKYSCFALFVKFGKEVAVKMKQYKDELLASCLTFLLSLPHNIIELDVRAYVPALQ
 FT MAFKLGLSYTPLAEVGLNALEEWISIYIDRHVMQPYKIDILPCLDGYLKTALSDETQNN
 FT WEVSALSRAAQKGFNKVVLKHLKKTKNLSSNEAISLEEIRIRVVQMLGSLGGQINKNLL
 FT TVTSSDEMMSYVAWDREKRLSFAVPPREMKPVIIFLDVFLPRVTELALTASDRQTKVAA
 FT CELLHSMVMFMLGKATQMPGEGGQAPPMYQLYKRTFPVLLRLACDQVTRQLYEPLVM
 FT QLIHWFTNNKKFESQDTVSLLEAILDGIIVDPVDSTLRDFCGRCIREFLKWSIKQITPQQ
 FT QEKSPVNTKSLFKRLYSLALHPNAFKRLGASLAFNNIYREFREEESLVEQFVFEALVY
 FT MESLALAHADEKSLGTIOCCDAIDHLCRIIEKKHVS LNKA KRRRLPRGFPPSASLCLL
 FT DLVKWLLAHCGRPQTECRHKSIELFYKFVPLLPGNRSPNLWLKDVLEEGVSFLINTFE
 FT GGGCGQPSGILAQPTLLYLGRPFSLQATLCWLDLLAALCEYNTFIGERTVGALQVLGT
 FT EAQSSLLKAVAFFLESIAMHDIIAAEKCFGTGAAGNRTSPQEGERYNSKCTVVVRIME
 FT FTTTLNTPSGWMLLKKDLCNTHLMRVLVQTLCEPASIGFNIGDVQVMAHLPDVCVNL
 FT MKALKMSPYKIDILETHLREKITAQSIEELCAVNLYGPDAQVDRSLAAVVSACKQLHRA
 FT GLLHNILPSQSTDLHHSVGTTELLSLVYKGIAPGDERQCLPSLDLSCKQLASGLLELFAFA
 FT FGGLCERLVSLLLNPAVLSTASLGSSQGSVHFSHGEYFYSLSFSETINTELLKNLDLAV
 FT LELMQSSVDNTKMSAVLNGMLDQSFREANQKHQGLKLATTILQHKKCDSWWAKDSP
 FT LETKMAVLALLAKILQIDSSVSFNTSHGSSFPEVFTTYISLLADTKLDLHKGQAVTLLP
 FT FFTSLTGGSLLELRRVLEQLIVAHFPMOSREFPEGTFRFNMYVDMKKFLDALELSQSP
 FT MLLELMTVELCREQQHVMELFQSSFRRIARRGSCVTQVGLLESVYEMFRKDDPRLSFT
 FT RQSFVDRSLTLLWHCSLDALREFSTIVVDAIDVLKSRFTKLNSTFDTQITKMGY
 FT KILDVMSRLPKDDVHAKESKINQVFGSCITEGNETKTILKLCYDAVNTMAGENQL
 FT LERRRLYHCAAYNCAISVICCVNELKFYQGFLFSEKPEKNLLIFENIDLKRRYNFPV
 FT EVEVPMERKQKYIEIRKEAREAAANGSDGPSYMSLSYLADSTLSEEMSQFDFSTGVQS
 FT YSYSSQDPRPATGRFRREQRDPTVHDDVLELEMDLNRHECMAPLTALVKHMHRSGLP
 FT PQGEEDSVPRDLPDPSWMKFLHGLKGNPVPNLNIRLFLAKLVINTEEVFRPYAKHWSLPLL
 FT QLAASENNGGEGIHVMVEIVATILSWTGLATPTGVPKDEVLANRLNLFMLKHVFHFKR
 FT AVFRHNLEI IKTLVECKWDCLSIPYRLIFEKFSGKDPNSKDNVSGIQLLGIVMANDLPP
 FT YDPQCGIQSSEYFQALVNMSFVRYKEVYAAAAEVLGLILRYVMERKNILEESLCELVA
 FT KQLKQHONTMEDKFIIVCLNKVTKSFPLADRFMNAVFFLLPKFHLNCLLEVVLKCRV
 FT EGMTLEYFOLKSKDFVQVMRHRDERQKVCLDIYKMPKLPVELRELINPVVEFVSHP
 FT STTCREOMYNILMWIHDNYRDPSETDNDSDQEIFKLAKDVLIQGLIDENPGLQIIRNF
 FT WSHETRLPSNTLDRLLALNSLYSPKIEVHFLSLATNLFLEMTSMSPDPYPMFHEPLSE
 FT CEFQEYTIIDSDWRSTVLTMPFVETQASQGLTQTRTQEGSLSARWPVAGQIRATQQQH
 FT DFTLTQTADGRSSFDTLWTSSTDPDLDHTSPSSDLSLFAHKSERLQRAPLKSVPDFG
 FT KKRLGLPGDEVNDKVKGAAGRTDLLRLRRRFMRDQEKLSLMYARKGVAEQKREKEIKSE
 FT LKMKQDAQVVLVRSYRHGDLDPDIQIKHSSLITPLQAVAQRPDIIAKQLFSSLSFGILKE
 FT MDKFKTLSEKNNTIKLQDENRFLNTTFSFFPPFVSCIQDISCQHAALLSLDPAVSA
 FT GCLASLQQFVGIRLLEALRLPLPAELPAKRVRGKARLPDVLRLWVELAKLYRSIGYD
 FT VLRGIFTSEIGTKQITQSALLAEARSDYSEAAKQYDEALNKQDWDGEPTEAEKDFWEL
 FT ASLDCYNHLAEWKSLEYCSTASIDSENPPDLNKIWSEPFYQETYLPMIRSKLKLLOG
 FT EADQSLTTFIDKAMHGELOKAILLEHYSQELSLLYLLQDDVDRAKYTIQNGIQSFQNY
 FT SSIDVLLHQSRITKLSQVQALTEIQEFISFISKQGNLSSQVPLKRLNLTWNNRYPDAM
 FT DPMNIWDDIITNRCFFLSKIEEKLTPPEDNSMNVDDQDPSDRMEVQEQEEDISSLR
 FT SCKFSMKMKMIDSARKQNNFSLAMKLLKELHKESTTRDVLVSWVQSYCRLSHCRSRSQ
 FT GCSEQVLTVLKTVSLDENNVSSYLXKNILAFRDQNTILGTTYRIANALSSEPACLAE
 FT IEEDKARRILELSSGSSSEDESEKVIAGLYQRAFOHLSEAVQAAEEEAQPPSWGCPAAGV
 FT IDAYMTLADFCDQQLRKEENASVTDSAELQAYPALVVEKMLKALKLNSNEARLKFPRL
 FT LQIITERYPEETLSLMTKEISSVPCWQFISWISHMVALLDKQAVAVQHSVEEITINYPQ
 FT AIVYFFIISSESYSKFDTSTGHKNKEFVARIKSKLDQGGVIQDFINALDQLSNPELLFK
 FT DWSNDVRAELAKTPVNKKNIKMYERMYAALGDPKAPGLGAFFRKFIQTFGKEFDKHFQ
 FT KGGSKLLRMKLSDFNDITNMLLLKMNKDSKPPGNLKECSPWMSDFKVEFLRNELEIPGQ
 FT YDGRGKPLPEYHVRLAGFDERVTVMASLRPKRIIRGHDEREHPFLVKGEDLRQDQR
 FT VBQLFQVMNGILAQDSACSQRALQLRTYSVVPMTSSDPRAPCEYKDWLTKMSGKHIDV
 FT AYMLMYKGANRTETVTSFRKRESKVPADLLKRAFVRMSTSPFAFLALRSHFASSHALIC
 FT ISHWILGIGDRHLANFMVAMETGGVIGIDFGHAFGSATQFLPVPPELMPFRLTRQFINLM
 FT LPMKETGLMYSIMVHALRAFRSDPGLLTNTIMDVFKESFDWKNFEQKMLKGGSWIQE
 FT INVAEKWYPRQKICYAKRKLAPANPAVITCDELLLGHEKAPAFRDYVAVARGSKDHNI
 FT RAQEPESGLSEETQVKCLMDQATDPNLTGRTWEGWEPWM*
 XX
 SQ Sequence 12780 BP; 3612 A; 2769 C; 3084 G; 3314 T; 1 other;

U34994 Length: 12780 July 10, 1998 12:15 Type: N Check: 8189 .. Figure 9b(1)

1 ATTTCCGGGT CCGGGCCGAG CGGGCGCAG CGGGGAGCG GGACTCGGCG

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Figure 9b (ii)

51 GCATGGCGGG CTCCGGAGCC GGTGTGCGTT GCTCCCTGCT GCGGCTGCAG
101 GAGACCTTGT CCGCTGCGGA CCGCTGCGGT GCTGCCCTGG CCGGTCATCA
151 ACTGATCCGC GGCCTGGGGC AGGAATGCGT CCTGAGCAGC AGCCCCGCGG
201 TGCTGGCATT ACAGACATCT TTAGTTTTTT CCAGAGATTT CGGTTTGCTT
251 GTATTTGTCC GGAAGTCACT CAACAGTATT GAATTTCTGT AATGTAGAGA
301 AGAAATCCTA AAGTTTTTAT GTATTTTCTT AGAAAAAATG GGCCAGAAGA
351 TCGCACCTTA CTCTGTTGAA ATTAAGAACA CTTGTACCAG TGTTTATACA
401 AAAGATAGAG CTGCTAAATG TAAAATTCCA GCCCTGGACC TTCTTATTAA
451 GTTACTTCAG ACTTTTAGAA GTTCTAGACT CATGGATGAA TTTAAAATTG
501 GAGAATTATT TAGTAAATTC TATGGAGAAC TTGCATTGAA AAAAAAATA
551 CCAGATACAG TTTTAGAAAA AGTATATGAG CTCCTAGGAT TATTGGGTGA
601 AGTTCATCCT AGTGAGATGA TAAATAATGC AGAAAACCTG TTCCGCGCTT
651 TTCTGGGTGA ACTTAAGACC CAGATGACAT CAGCAGTAAG AGAGCCCAAA
701 CTACCTGTTT TGGCAGGATG TCTGAAGGGG TTGTCCTCAC TTCTGTGCAA
751 CTTCACTAAG TCCATGGAAG AAGATCCCCA GACTTCAAGG GAGATTTTTA
801 ATTTTGTACT AAAGGCAATT CGTCCTCAGA TTGATCTGAA GAGATATGCT
851 GTGCCCTCAG CTGGCTTGCG CCTATTTGCC CTGCATGCAT CTCAGTTTAG
901 CACCTGCCTT CTGGACAAC ACGTGCTCTT ATTTGAAGTC TTGTTAAAGT
951 GGTGTGCCCA CACAAATGTA GAATTGAAAA AAGCTGCACT TTCAGCCCTG
1001 GAATCCTTTC TGAAACAGGT TTCTAATATG GTGGCGAAAA ATGCAGAAAT
1051 GCATAAAAAAT AAAGTGCAGT ACTTTATGGA GCAGTTTTAT GGAATCATCA
1101 GAAATGTGGA TTCGAACAAC AAGGAGTTAT CTATTGCTAT CCGTGGATAT
1151 GGACTTTTTG CAGGACCGTG CAAGGTTATA AACGCAAAAG ATGTTGACTT
1201 CATGTACGTT GAGCTCATT AGCGCTGCAA GCAGATGTTT CTCACCCAGA
1251 CAGACACTGG TGACTACCGT GTTTATCAGA TGCCAAGCTT CCTCCAGTCT
1301 GTTGCAAGCG TCTTGCTGTA CCTTGACACA GTTCCTGAGG TGTATACTCC
1351 AGTTCTGGAG CACCTCGTGG TGATGCAGAT AGACAGTTTC CCACAGTACA
1401 GTCCAAAAAT GCAGCTGGTG TGTGTCAGAG CCATAGTGAA GGTGTTCTTA
1451 GCTTTGGCAG CAAAAGGGCC AGTTCTCAGG AATTGCATTA GTACTGTGGT
1501 GCATCAGGGT TTAATCAGAA TATGTTCTAA ACCAGTGGTC CTTCCAAAGG
1551 GCCCTGAGTC TGAATCTGAA GACCACCGTG CTTCAGGGGA AGTCAGAACT
1601 GGCAAATGGA AGGTGCCCAC ATACAAAGAC TACGTGGATC TCTTCAGACA
1651 TCTCCTGAGC TCTGACCAGA TGATGGATT CTTTTAGCA GATGAAGCAT

Figure 9b (111)

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1701 TTTTCTCTGT GAATTCCTCC AGTGAAAGTC TGAATCATTT ACTTTATGAT
1751 GAATTTGTAA AATCCGTTTT GAAGATTGTT GAGAAATTGG ATCTTACACT
1801 TGAAATACAG ACTGTTGGGG AACAAAGAGAA TGGAGATGAG GCGCCTGGTG
1851 TTTGGATGAT CCCAACTTCA GATCCAGCGG CTAACCTGCA TCCAGCTAAA
1901 CCTAAAGATT TTTGCGCTTT CATTAACCTG GTGGAATTTT GCAGAGAGAT
1951 TCTCCCTGAG AAACAAGCAG AATTTTTTTGA ACCATGGGTG TACTCATTTT
2001 CATATGAATT AATTTTGCAA TCTACAAGGT TGCCCTCAT CAGTGGTTTC
2051 TACAAATTGC TTTCTATTAC AGTAAGAAAT GCCAAGAAAA TAAAATATTT
2101 CGAGGGAGTT AGTCCAAAGA GTCTGAAACA CTCTCCTGAA GACCCAGAAA
2151 AGTATTCTTG CTTTGCTTTA TTTGTGAAAT TTGGCAAAGA GGTGGCAGTT
2201 AAAATGAAGC AGTACAAAGA TGAACCTTTTG GCCTCTTGTT TGACCTTTCT
2251 TCTGTCCTTG CCACACAACA TCATTGAACT CGATGTTAGA GCCTACGTTT
2301 CTGCACTGCA GATGGCTTTC AAACCTGGCC TGAGCTATAC CCCCTTGGCA
2351 GAAGTAGGCC TGAATGCTCT AGAAGAATGG TCAATTTATA TTGACAGACA
2401 TGTAATGCAG CCTTATTACA AAGACATTCT CCCCTGCCTG GATGGATACC
2451 TGAAGACTTC AGCCTTGCTCA GATGAGACCA AGAATAACTG GGAAGTGCTA
2501 GCTCTTTCTC GGGCTGCCCA GAAAGGATTT AATAAAGTGG TGTAAAGCA
2551 TCTGAAGAAG ACAAAGAACC TTTCATCAAA CGAAGCAATA TCCTTAGAAG
2601 AAATAAGAAT TAGAGTAGTA CAAATGCTTG GATCTCTAGG AGGACAAATA
2651 AACAAAAATC TTCTGACAGT CACGTCCTCA GATGAGATGA TGAAGAGCTA
2701 TGTGGCCTGG GACAGAGAGA AGCGGCTGAG CTTTGCACTG CCCTTTAGAG
2751 AGATGAAACC TGTCATTTTT CTGGATGTGT TCCTGCCTCG AGTCACAGAA
2801 TTAGCGCTCA CAGCCAGTGA CAGACAACT AAAGTTGCAG CCTGTGAACT
2851 TTTACATAGC ATGGTTATGT TTATGTTGGG CAAAGCCACG CAGATGCCAG
2901 AAGGGGGACA GGGAGCCCCA CCCATGTACC AGCTCTATAA GCGGACGTTT
2951 CCTGTGCTGC TTOGACTTGC GTGTGATGTT GATCAGGTGA CAAGGCAACT
3001 GTATGAGCCA CTAGTTATGC AGCTGATTCA CTGGTTCACT AACAACAAGA
3051 AATTTGAAAG TCAGGATACT GTTTCCTTAC TAGAAGCTAT ATTGGATGGA
3101 ATTGTGGACC CTGTTGACAG TACTTTAAGA GATTTTTGTG GTCGGTGTAT
3151 TCGAGAATTC CTTAAATGGT CCATTAAGCA AATAACACCA CAGCAGCAGG
3201 AGAAGAGTCC AGTAAACACC AAATCGCTTT TCAAGCGACT TTATAGCCTT
3251 GCGCTTCACC CCAATGCTTT CAAGAGGCTG GGAGCATCAC TTGCCTTTAA
3301 TAATATCTAC AGGGAATTCA GGGGAAGAAGA GTCTCTGGTG GAACAGTTTG
3351 TGTTTGAAGC CTTGGTGATA TACATGGAGA GTCTGGCCTT AGCACATGCA

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Figure 9b (iv)

3401 GATGAGAAGT CCTTAGGTAC AATTCAACAG TGTGTGATG CCATTGATCA
3451 CCTATGCCGC ATCATTGAAA AGAAGCATGT TTCTTTAAAT AAAGCAAAGA
3501 AACGACGTTT GCCGCGAGGA TTTCACCTT CCGCATCATT GTGTTTATTG
3551 GATCTGGTCA AGTGGCTTTT AGCTCATTGT GGGAGGCCCC AGACAGAATG
3601 TCGACACAAA TCCATTGAAC TCTTTTATAA ATTCGTTTCTT TTATTGCCAG
3651 GCAACAGATC CCCTAATTG TGGCTGAAAG ATGTTCTCAA GGAAGAAGGT
3701 GTCTCTTTTC TCATCAACAC CTTTGAGGGG GGTGGCTGTG GCCAGCCCTC
3751 GGGCATCCTG GCCCAGCCCA CCCTCTTGTA CCTTCGGGGG CCATTGAGCC
3801 TGCAGGCCAC GCTATGCTGG CTGGACCTGC TCCTGGCCGC GTTGGAGTGC
3851 TACAACACGT TCATTGGCGA GAGAACTGTA GGAGCGCTCC AGGTCCTAGG
3901 TACTGAAGCC CAGTCTTAC TTTTGAAAGC AGTGGCTTTC TTCTTAGAAA
3951 GCATTGCCAT GCATGACATT ATAGCAGCAG AAAAGTGCTT TGGCACTGGG
4001 GCAGCAGGTA ACAGAACAAG CCCACAAGAG GGAGAAAGGT ACAACTACAG
4051 CAAATGCACC GTTGTGGTCC GGATTATGGA GTTTACCACG ACTCTGCTAA
4101 ACACCTCCCC GGAAGGATGG AAGCTCCTGA AGAAGGACTT GTGTAATACA
4151 CACCTGATGA GAGTCCTGGT GCAGACGCTG TGTGAGCCCG CAAGCATAGG
4201 TTTCAACATC GGAGACGTCC AGGTTATGGC TCATCTTCCT GATGTTTGTG
4251 TGAATCTGAT GAAAGCTCTA AAGATGTCCC CATACAAAGA TATCCTAGAG
4301 ACCCATCTGA GAGAGAAAAT AACAGCACAG AGCATTGAGG AGCTTTGTGC
4351 CGTCAACTTG TATGGCCCTG ACGCGCAAGT GGACAGGAGC AGGCTGGCTG
4401 CTGTTGTGTC TGCCGTGAAA CAGCTTCACA GAGCTGGGCT TCTGCATAAT
4451 ATATTACCGT CTCAGTCCAC AGATTTGCAT CATTCTGTTG GCACAGAACT
4501 TCTTTCCCTG GTTTATAAAG GCATTGCCCC TGGAGATGAG AGACAGTGTG
4551 TGCCCTTCTCT AGACCTCAGT TGTAAGCAGC TGGCCAGCGG ACTTCTGGAG
4601 TTAGCCTTTG CTTTGGAGG ACTGTGTGAG CGCCTTGTA GTCTCTCTCT
4651 GAACCCAGCG GTGCTGTCCA CGGCGTCCCT GGGCAGCTCA CAGGGCAGCG
4701 TCATCCACTT CTCCCATGGG GAGTATTTCT ATAGCTTGTT CTCAGAAACG
4751 ATCAACACGG AATTATTGAA AAATCTGGAT CTGCTGTAT TGGAGCTCAT
4801 GCAGTCTTCA GTGGATAATA CCAAAATGGT GAGTGCCGTT TTGAACGGCA
4851 TGTTAGACCA GAGCTTCAGG GAGCGAGCAA ACCAGAAACA CCAAGGACTG
4901 AAACCTGCGA CTACAATTCT GCAACACTGG AAGAAGTGTG ATTCAATGGT
4951 GGCCAAAGAT TCCCTCTCG AAATAAAAT GGCAGTGCTG GCCTTACTGG
5001 CAAAAATTTT ACAGATTGAT TCATCTGTAT CTTTAAATAC AAGTCATGGT

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Figure 9b (v)

5051 TCATCCCTG AAGTCTTTAC AACATATATT AGTCTACTTG CTGACACAAA
5101 GCTGGATCTA CATTTAAGG GCCAAGCTGT CACTCTTCTT CCATTCTTCA
5151 CCAGCCTCAC TGGAGGCAGT CTGGAGGAAC TTAGACGTGT TCTGGAGCAG
5201 CTCATCGTTG CTCACTTCCC CATGCAGTCC AGGGAATTTT CTCCAGGAAC
5251 TCCGCGGTTT AATAATTATG TGGACTGCAT GAAAAAGTTT CTAGATGCAT
5301 TGGAATTATC TCAAAGCCCT ATGTTGTTGG AATTGATGAC AGAAGTTCTT
5351 TGTGCGGAAC AGCAGCATGT CATGGAAGAA TTATTTCAAT CCAGTTTCAG
5401 GAGGATTGCC AGAAGGGGTT CATGTGTCAC ACAAGTAGGC CTTCTGGAAA
5451 GCGTGATGA AATGTTTCAAG AAGGATGACC CCCGCCTAAG TTTACACGC
5501 CAGTCTTTTG TGGACCGCTC CCTCCTCACT CTGCTGTGGC ACTGTAGCCT
5551 GGATGCTTTG AGAGAATTCT TCAGCACAAT TGTGGTGGAT GCCATTGATG
5601 TGTTGAAGTC CAGGTTTACA AAGCTAAATG AATCTACCTT TGATACTCAA
5651 ATCACCAAGA AGATGGGCTA CTATAAGATT CTAGACGTGA TGTATTCTCG
5701 CCTTCCCAA GATGATGTTT ATGCTAAGGA ATCAAAAATT AATCAAGTTT
5751 TCCATGGCTC GTGTATTACA GAAGGAAATG AACTTACAAA GACATTGATT
5801 AAATTGTGCT ACGATGCATT TACAGAGAAC ATGGCAGGAG AGAATCAGCT
5851 GCTGGAGAGG AGAAGACTTT ACCATTGTGC AGCATACAAC TGCGCCATAT
5901 CTGTCACTG CTGTGTCTTC AATGAGTTAA AATTTTACCA AGGTTTTCTG
5951 TTTAGTGAAA AACCAGAAAA GAAGTTGCTT ATTTTGTAAA ATCTGATCGA
6001 CCTGAAGCGC CGCTATAATT TTCTGTAGA AGTTGAGGTT CCTATGGAAA
6051 GAAAGAAAA GTACATTGAA ATTAGGAAAG AAGCCAGAGA AGCAGCAAAT
6101 GGGGATTGAG ATGGTCTTTC CTATATGTCT TCCCTGTCTAT ATTTGGCAGA
6151 CAGTACCTTG AGTGAGGAAA TGAGTCAATT TGATTTCTCA ACCGGAGTTC
6201 AGAGCTATT ATACAGCTCC CAAGACCCTA GACCTGCCAC TGGTCGTTTT
6251 CGGAGACGGG AGCAGCGGGA CCCCACGGTG CATGATGATG TGCTGGAGCT
6301 GGAGATGGAC GAGCTCAATC GGCATGAGTG CATGGCGGCC CTGACGGGCC
6351 TGGTCAAGCA CATGCACAGA AGCCTGGGCC CGCCTCAAGG AGAAGAGGAT
6401 TCAGTGCCAA GAGATCTTCC TTCTTGATG AAATTCCTCC ATGGCAAAT
6451 GGGAAATCCA ATAGTACCAT TAAATATCCG TCTCTTCTTA GCCAAGCTTG
6501 TTATTAATAC AGAAGAGGTC TTTCGCCCTT ACGCGAAGCA CTGGCTTAGC
6551 CCTTGCTGC AGCTGGCTGC TTCTGAAAC AATGGAGGAG AAGGAATTCA
6601 CTACATGGTG GTTGAGATAG TGGCCACTAT TCTTTTCATG ACAGGCTTGG
6651 CCACTCCAAC AGGGGTCCCT AAAGATGAAG TGTTAGCAA TCGATTGCTT
6701 AATTTCTTAA TGAAACATGT CTTTCATCCA AAAAGAGCTG TGTTTAGACA

Figure 9b (vi)

6751 CAACCTTGAA ATTATAAAGA CCCTTGTCGA GTGCTGGAAG GATTGTTTAT
6801 CCATCCCTTA TAGGTTAATA TTTGAAAAGT TTTCCGGTAA AGATCCTAAT
6851 TCTAAAGACA ACTCAGTAGG GATTCAATTG CTAGGCATCG TGATGGCCAA
6901 TGACCTGCCT CCCTATGACC CACAGTGTGG CATCCAGAGT AGCGAATACT
6951 TCCAGGCTTT GGTGAATAAT ATGTCCTTTG TAAGATATAA AGAAGTGTAT
7001 GCCGCTGCAG CAGAAGTTCT AGGACTTATA CTTCGATATG TTATGGAGAG
7051 AAAAAACATA CTGGAGGAGT CTCTGTGTGA ACTGGTTGCG AAACAATTGA
7101 AGCAACATCA GAATACTATG GAGGACAAGT TTATTGTGTG CTTGAACAAA
7151 GTGACCAAGA GCTTCCCTCC TCTTGCAGAC AGGTTTCATGA ATGCTGTGTT
7201 CTCTCTGCTG CCAAAATTTC ATGGAGTGTT GAAAACACTC TGTCTGGAGG
7251 TGGTACTTTG TCGTGTGGAG GGAATGACAG AGCTGTACTT CCAGTTAAAG
7301 AGCAAGGACT TCGTTCAAGT CATGAGACAT AGAGATGAAA GACAAAAAGT
7351 ATGTTTGGAC ATAATTTATA AGATGATGCC AAAGTTAAAA CCAGTAGAAC
7401 TCCGAGAACT TCTGAACCCC GTTGTGGAAT TCGTTTCCCA TCCTTCTACA
7451 ACATGTAGGG AACAAATGTA TAATATTCTC ATGTGGATTG ATGATAATTA
7501 CAGAGATCCA GAAAGTGAGA CAGATAATGA CTCCCAGGAA ATATTTAAGT
7551 TGGCAAAAGA TGTGCTGATT CAAGGATTGA TCGATGAGAA CCCTGGACTT
7601 CAATTAATTA TTCGAAATTT CTGGAGCCAT GAAACTAGGT TACCTTCAAA
7651 TACCTTGGAC CGGTGCTGG CACTAAATTC CTTATATTCT CCTAAGATAG
7701 AAGTGCAC TTAAAGTTTA GCAACAAATT TTCTGCTCGA AATGACCAGC
7751 ATGAGCCCAG ATTATCCAAA CCCCATGTTT GAGCATCCTC TGTGAGAATG
7801 CGAATTTTCA GAATATACCA TTGATTCTGA TTGGCGTTTC CGAAGTACTG
7851 TTCTCACTCC GATGTTTGTG GAGACCCAGG CCTCCCAGGG CACTCTCCAG
7901 ACCCGTACCC AGGAAGGGTC CCTCTCAGCT CGCTGGCCAG TGGCAGGGCA
7951 GATAAGGGCC ACCCAGCAGC AGCATGACTT CACACTGACA CAGACTGCAG
8001 ATGGAAGAAG CTCATTTGAT TGGCTGACCG GGAGCAGCAC TGACCCGCTG
8051 GTCGACCACA CCAGTCCCTC ATCTGACTCC TTGCTGTTTG CCCACAAGAG
8101 GAGTGAAAGG TTACAGAGAG CACCCTTGAA GTCAGTGGGG CCTGATTTTG
8151 GGAAAAAAG GCTGGGCCTT CCAGGGGACG AGGTGGATAA CAAAGTGAAA
8201 GGTGCGGCCG GCCGGACGGA CCTACTACGA CTGCGCAGAC GGTTTATGAG
8251 GGACCAGGAG AAGCTCAGTT TGATGTATGC CAGAAAAGGC GTTGCTGAGC
8301 AAAAAAGAGA GAAGGAAATC AAGAGTGAGT TAAAAATGAA GCAGGATGCC
8351 CAGGTGTTT TGTACAGAAG CTACCGGCAC GGAGACCTTC CTGACATTCA

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Figure 9b (v11)

8401 GATCAAGCAC AGCAGCCTCA TCACCCCGTT ACAGGCCGTG GCCCAGAGGG
 8451 ACCCAATAAT TGCAAAACAG CTCTTTAGCA GCTTGTTTTTC TGGAATTTTG
 8501 AAAGAGATGG ATAAATTTAA GACACTGTCT GAAAAAACA ACATCACTCA
 8551 AAAGTTGCTT CAAGACTTCA ATCGTTTTCT TAATACCACC TTCTCTTTCT
 8601 TTCCACCCCTT TGTCTCTTGT ATTGAGGACA TTAGCTGTCA GCACGCAGCC
 8651 CTGCTGAGCC TCGACCCAGC GGCTGTTAGC GCTGGTTGCC TGGCCAGCCT
 8701 ACAGCAGCCC GTGGGCATCC GCCTGCTAGA GGAGGCTCTG CTCCGCCTGC
 8751 TGCCTGCTGA GCTGCCTGCC AAGCGAGTCC GTGGGAAGGC CCGCCTCCCT
 8801 CCTGATGTCC TCAGATGGGT GGAGCTTGCT AAGCTGTATA GATCAATTGG
 8851 AGAATACGAC GTCCTCCGTG GGATTTTTAC CAGTGAGATA GGAACAAAGC
 8901 AAATCACTCA GAGTGCATTA TTAGCAGAAG CCAGAAGTGA TTATTTCTGAA
 8951 GCTGCTAAGC AGTATGATGA GGCTCTCAAT AAACAAGACT GGGTAGATGG
 9001 TGAGCCCAACA GAAGCCGAGA AGGATTTTTG GGAAGTTGCA TCCCTTGACT
 9051 GTTACAACCA CCTTGCTGAG TGGAAATCAC TTGAATACTG TTCTACAGCC
 9101 AGTATAGACA GTGAGAACCC CCCAGACCTA AATAAAATCT GGAGTGAACC
 9151 ATTTTATCAG GAAACATATC TACCTTACAT GATCCGCAGC AAGCTGAAGC
 9201 TGCTGCTCCA GGGAGAGGCT GACCAGTCCC TGCTGACATT TATTGACAAA
 9251 GCTATGCACG GGGAGCTCCA GAAGGCGATT CTAGAGCTTC ATTACAGTCA
 9301 AGAGCTGAGT CTGCTTTACC TCCTGCAAGA TGATGTTGAC AGAGCCAAAT
 9351 ATTACATTCA AAATGGCATT CAGAGTTTCA TGCAGAATTA TTCTAGTATT
 9401 GATGTCCCTCT TACACCAAAG TAGACTCACC AAATTGCAGT CTGTACAGGC
 9451 TTTAACAGAA ATTCAGGAGT TCATCAGCTT TATAAGCAAA CAAGGCAATT
 9501 TATCATCTCA AGTTCCCTTT AAGAGACTTC TGAACACCTG GACAAACAGA
 9551 TATCCAGATG CTAAAATGGA CCCAATGAAC ATCTGGGATG ACATCATCAC
 9601 AAATCGATGT TTCTTTCTCA GCAAAATAGA GGAGAAGCTT ACCCCTCTTC
 9651 CAGAAGATAA TAGTATGAAT GTGGATCAAG ATGGAGACCC CAGTGACAGG
 9701 ATGGAAGTGC AAGAGCAGGA AGAAGATATC AGCTCCCTGA TCAGGAGTTG
 9751 CAAGTTTTTC ATGAAAATGA AGATGATAGA CAGTGCCCGG AAGCAGAACA
 9801 ATTTCTCACT TGCTATGAAA CTACTGAAGG AGCTGCATAA AGAGTCAAAA
 9851 ACCAGAGACG ATTGGCTGGT GAGCTGGGTG CAGAGCTACT GCCGCCTGAG
 9901 CCACTGCCCG AGCCCGTCCC AGGGCTGCTC TGAGCAGGTG CTCACTGTGC
 9951 TGAAAACAGT CTCTTTGTTG GATGAGAACA ACGTGTCAAG CTACTTAARC
 10001 AAAAATATTC TGGCTTTCCG TGACCAGAAC ATTCTCTTGG GTACAACTTA
 10051 CAGGATCATA GCGAATGCTC TCAGCAGTGA GCCAGCCTGC CTTGCTGAAA

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Fig.10.

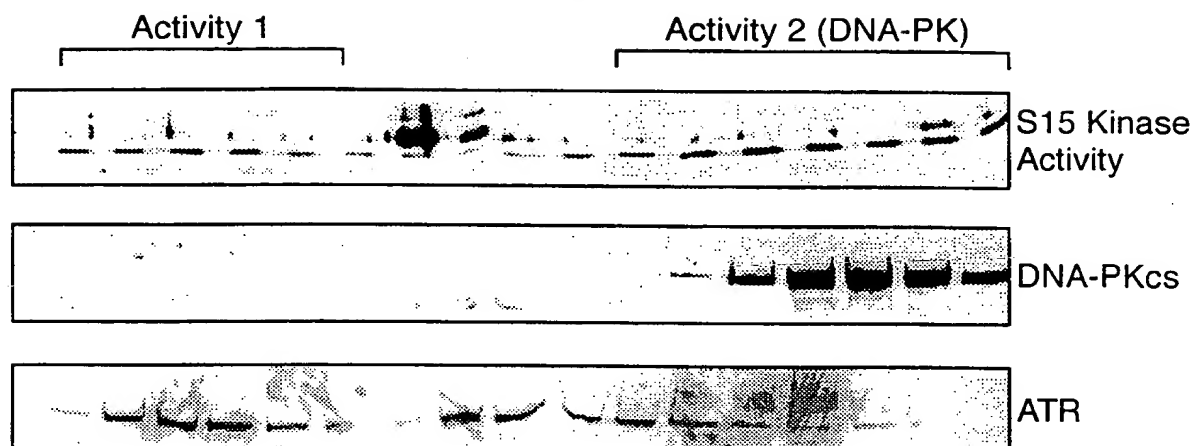


Fig.11.

